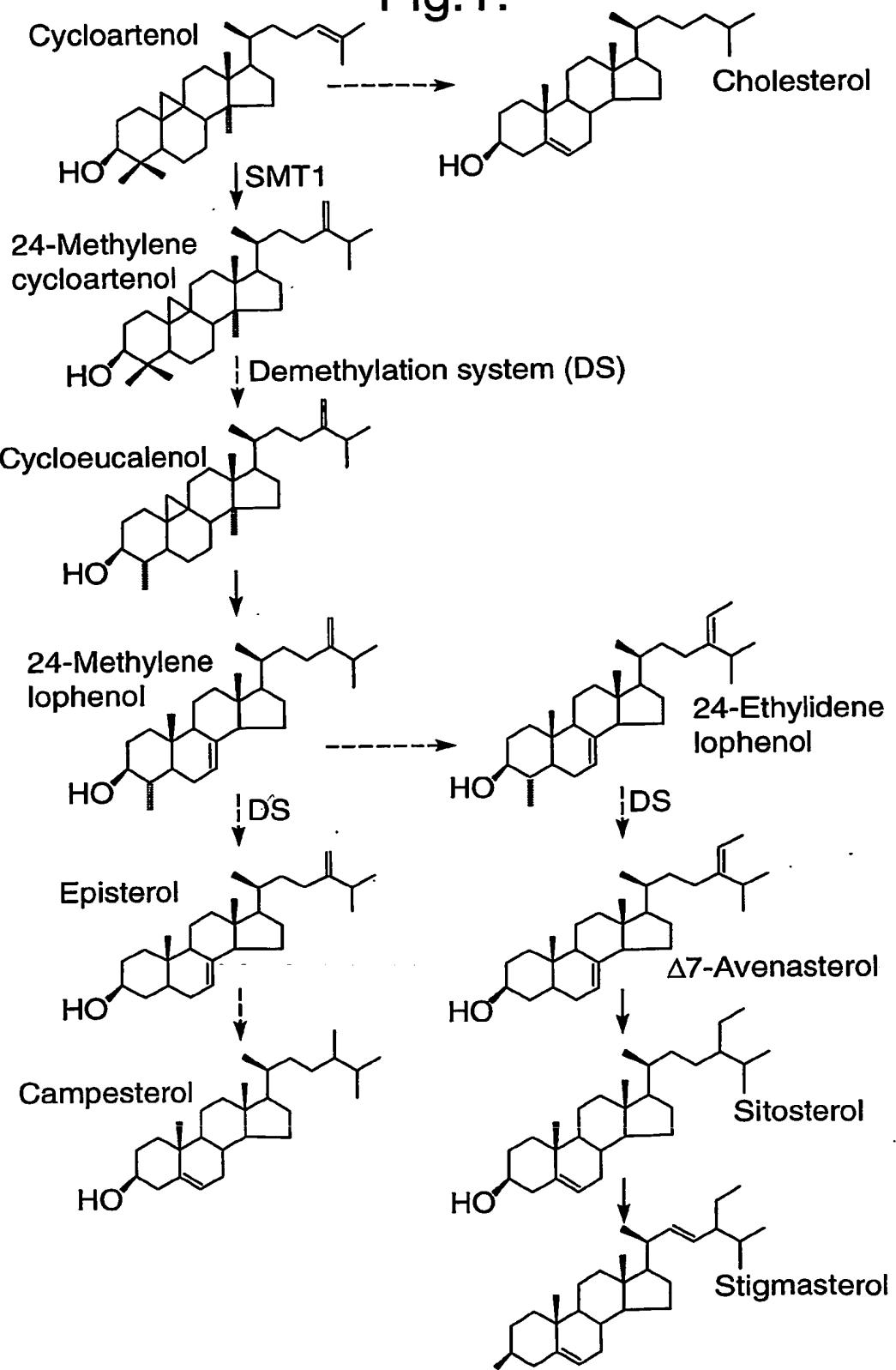


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Fig.1.



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Fig.2.

1 ATGCAGTACC TTGTTACGCA TTTCACTGG CGTGTATTGG GAGTTTATA
 M Q Y L V T H F S D F Q L A C I G S F I
 61 CTTCATGAAA GCGTGTTTT CTTGTCTGGA CTCCCTTACA TTTTCCTAGA AAGGACTGGT
 L H E S V F F L S G L P Y I F L E R T G
 121 TTTCTGAGCA ACTACAAAAT TCAGACCAAA AGTAATACTC CTGAAGCCCA GGGAAAATGC
 F L S N Y K I Q T K S N T P E A Q G K C
 181 ATTGCTCGAC TATTACTTTA CCATTGCTGC GTAAACCTGC CCCTCATGAT GGCGTCGTAT
 I A R L L L Y H C C V N L P L M M A S Y
 241 CCTGTATTCA GATTCACTGGG CATGGAAAGC AGTTTCCTC TGCCGTCCTG GAAAGTGGTG
 P V F R F M G M E S S F P L P S W K V V
 301 TCTGCCAGA TCTTATTCTA CTTCATCATT GAGGATTTG TATTCTATTG GGTCACAGG
 S A Q I L F Y F I I E D F V F Y W G H R
 361 ATCTTGATA CTAAATGGCT CTACAAGAAC GTGCACAGTG TGCACTCATGA GTACGCGACA
 I L H T K W L Y K N V H S V H H E Y A T
 421 CCGTTTGGTT TGACATCAGA ATATGCTCAT CCCGCTGAAA TTCTGTTCT TGTTTTGCT
 P F G L T S E Y A H P A E I L F L G F A
 481 ACCATTGTTG GTCCGGCTCT CACCGGGCCT CACCTGATCA CCCTTTGGTT ATGGATGATG
 T I V G P A L T G P H L I T L W L W M M
 541 CTCAGAGTTA TTGAGACAGT TGAGGCACAT TGTTGTTATC ATTTCCCAG GAGCCCCCTG
 L R V I E T V E A H C G Y H F P W S P S
 601 AATTTTCTTC CTCTATACGG CGGTGCTGAC TTCCATGACT ACCATCATCG ATTACTCTAC
 N F L P L Y G G A D F H D Y H H R L L Y
 661 ACAAAAGTCTG GCAACTACTC ATCAACGTTT GTTACATGG ACTGGATCTT TGGCACCGAT
 T K S G N Y S S T F V Y M D W I F G T D
 721 AAAGGTTACA GAAAACCTAA GGCCCTAAAA GAAACCTGA
 K G Y R K L K A L K E T -

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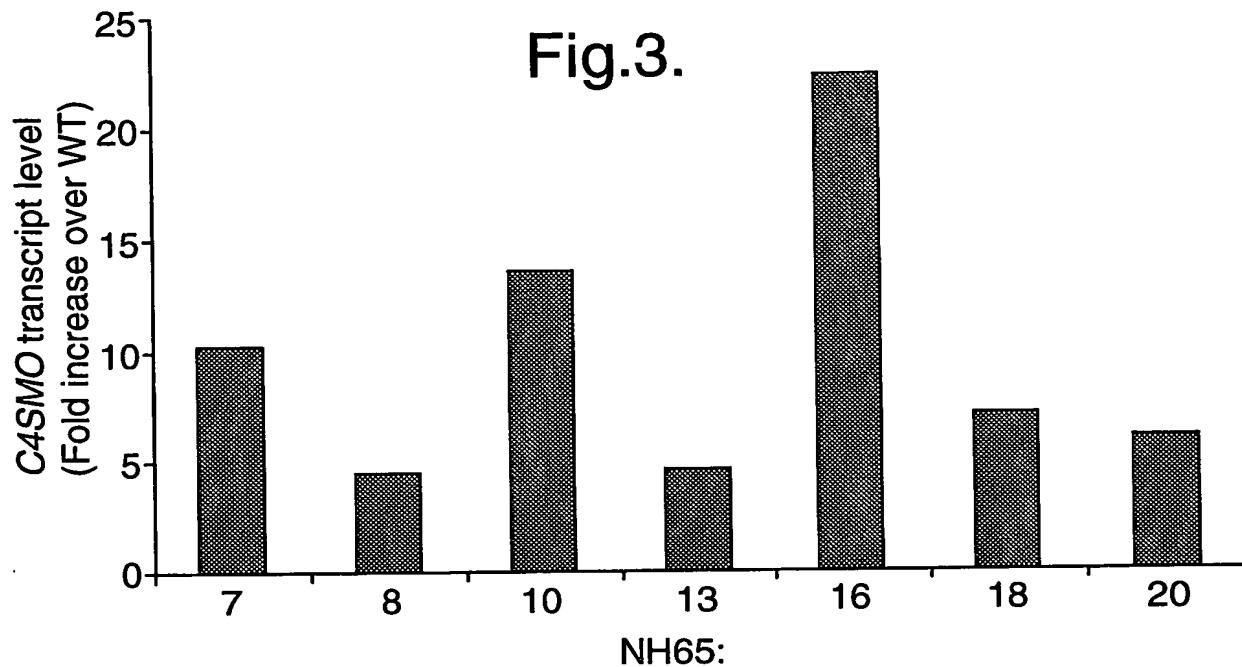
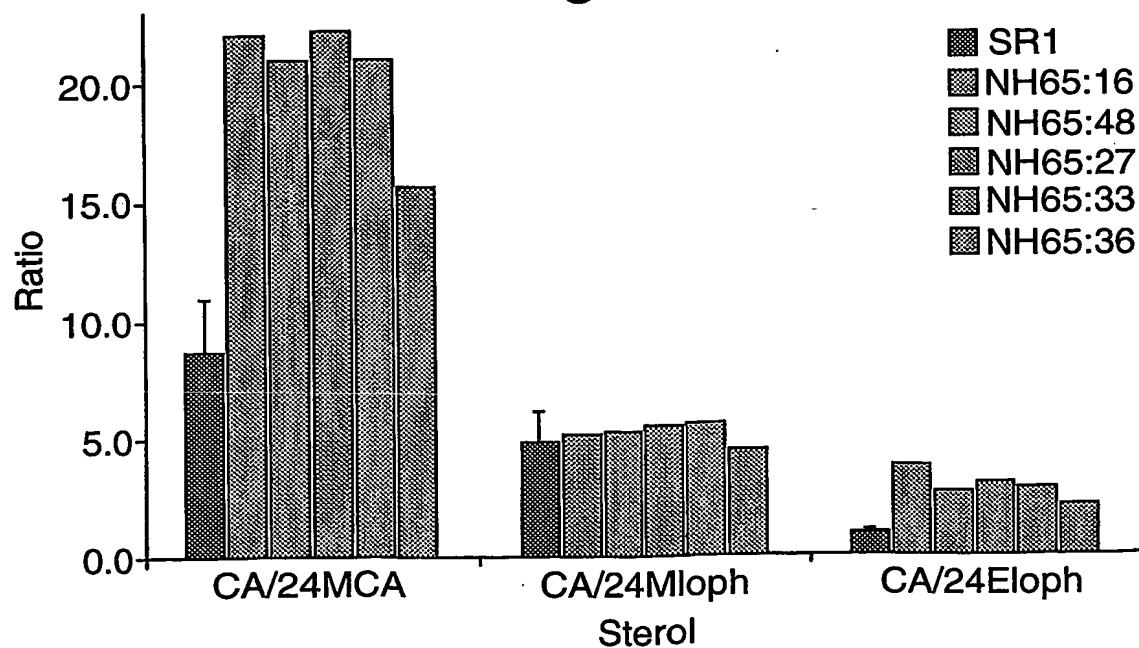
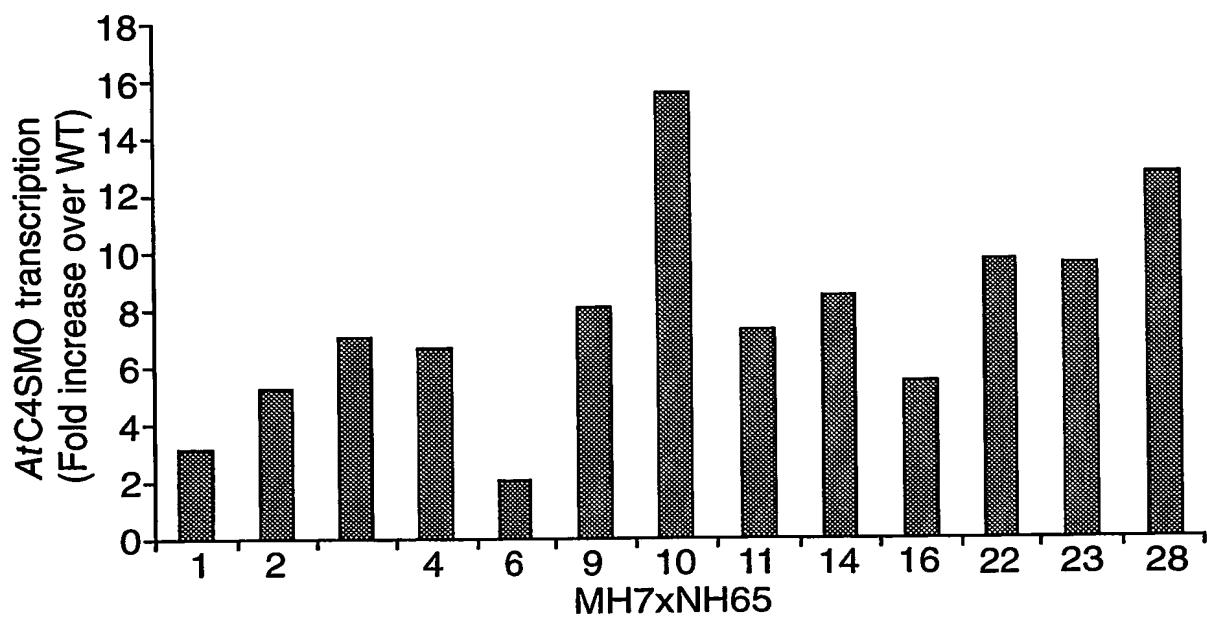


Fig.4.



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Fig.5.



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Fig.6A.

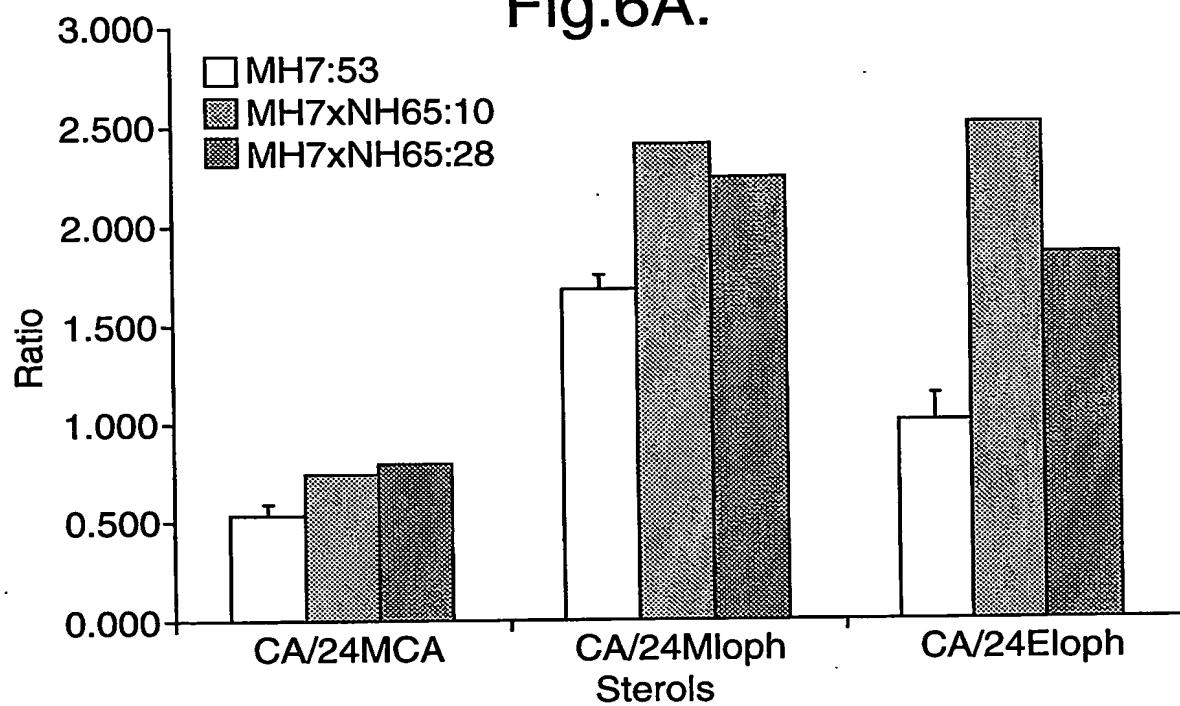


Fig.6B.

